WEST Search History

DATE: Friday, October 25, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR			
L6	L5 and random	271	L6
L5	L3 and overlap$5 adj5 sequence	283	L5
L4	L3 and overlap$5 adj5 random adj5 sequence	0	L4
L3	L2 and libr$5	1245	L3
L2	zinc adj4 finger	2012	L2
DB=USPT; PLUR=YES; OP=OR			
L1	zinc adj4 finger	1124	L1

END OF SEARCH HISTORY

result in loss of user privileges and other penalties.

* * * * * * * * * * * * * * STN Columbus * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 15:34:16 ON 25 OCT 2002

=> file ca
COST IN U.S. DOLLARS

	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.21	0.21

FILE 'CA' ENTERED AT 15:34:24 ON 25 OCT 2002
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE COVERS 1907 - 24 Oct 2002 VOL 137 ISS 18
FILE LAST UPDATED: 24 Oct 2002 (20021024/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

CAS roles have been modified effective December 16, 2001. Please check your SDI profiles to see if they need to be revised. For information on CAS roles, enter HELP ROLES at an arrow prompt or use the CAS Roles thesaurus (/RL field) in this file.

```
=> s zinc finger polypeptide
        436515 ZINC
         13451 FINGER
         86733 POLYPEPTIDE
L1          10 ZINC FINGER POLYPEPTIDE
               (ZINC(W)FINGER(W)POLYPEPTIDE)

=> s libra?(5w)zinc(4w)finger(4w)(peptide or polypeptide or Zif268 or tramtrack)
         65223 LIBRA?
        436515 ZINC
         13451 FINGER
        273453 PEPTIDE
         86733 POLYPEPTIDE
           283 ZIF268
            75 TRAMTRACK
L2           3 LIBRA?(5W)ZINC(4W)FINGER(4W)(PEPTIDE OR POLYPEPTIDE OR ZIF268
              OR TRAMTRACK)

=> d l2 1-3 ti au so py ab

L2   ANSWER 1 OF 3  CA  COPYRIGHT 2002 ACS
TI   Peptide libraries containing zinc finger variants and their use in
     selecting zinc fingers with defined binding specificities
```

IN Hine, Anna Victoria; Morgan, Leonie Jane; Santos, Albert Francis; Palfrey, David
SO PCT Int. Appl., 48 pp.
CODEN: PIXXD2
PY 2000
2001
AB Libraries of peptides that can be used to select nucleotide sequence-specific binding peptides are described. The peptides are based around zinc finger motifs and have invariant amino acids at those sites essential for zinc finger formation and alternative residues at sites involved in sequence-specific binding. The libraries, typically 6-20, can be used to identify sequence-specific ligands and the principles underlying sequence-specificity. A method of identifying a protein which interacts with a specific binding partner, which method comprises incubating the protein with each library of the set of libraries of proteins, observing specific binding interactions with certain libraries of the set, and using the observations to identify a protein which interacts with the specific binding partner. Gene libraries encoding these peptide libraries and a method of making a library of randomized genes encoding these peptides are described.

L2 ANSWER 2 OF 3 CA COPYRIGHT 2002 ACS
TI Design of nucleic acid-binding zinc finger polypeptide library
IN Choo, Yen; Klug, Aaron; Isalan, Mark
SO PCT Int. Appl., 56 pp.
CODEN: PIXXD2
PY 1998
1998
2001
2000
2002
AB The invention relates to a zinc finger polypeptide library in which each polypeptide comprises more than one zinc finger which has been at least partially randomized, and to a set of zinc finger polypeptide **libraries** which encode overlapping **zinc finger** polypeptides, each **polypeptide** comprising more than one zinc finger which has been at least partially randomized, and which polypeptides may be assembled after selection to form a multifinger zinc finger polypeptide. The design of zinc finger polypeptides recognizes the importance of overlapping 4-bp subsite recognition with the resultant synergy between zinc fingers, which is overlooked in classical zinc finger library design in which only a single zinc finger is randomized in each library. Further randomization is limited to substituting amino acids which are known to dictate variation in binding site specificity. A code of amino acid position bias is provided which permits the selection of the library against any nucleic acid sequence as the target sequence, and the prodn. of a specific nucleic acid-binding protein which will bind thereto. Moreover, a method is provided by which a zinc finger protein specific for any given nucleic acid sequence may be designed and optimized. A binary library system is constructed in which each library encodes the 3 fingers of Zip268 but with some amino acid positions selectively randomized. Instead of adhering to the model of modular zinc fingers, the new libraries contain concerted variations in certain amino acid positions in adjacent zinc fingers. Selection are performed using the DNA sequences GCG-GMN-OPQ and IJK-LMG-GCG.

L2 ANSWER 3 OF 3 CA COPYRIGHT 2002 ACS
TI Surface plasmon resonance based kinetic studies of zinc finger-DNA interactions
AU Yang, Wei-Ping; Wu, Herren; Barbas, Carlos F. III
SO Journal of Immunological Methods (1995), 183(1), 175-82
CODEN: JIMMBG; ISSN: 0022-1759
PY 1995
AB **Libraries** of the **zinc finger** DNA binding

protein, **Zif268**, were constructed and selected for affinity and specificity toward DNA targets using the phage display technique. Mutant proteins were purified to homogeneity and were characterized for their ability to interact with their DNA targets using a real-time biomol. interaction assay (BIA). One mutant protein, C7, bound the Zif268 consensus binding sequence with a 13-fold increase in affinity as compared to the wild-type Zif268 protein. Mutant proteins with moderate affinity for new DNA targets within a consensus sequence of HIV-1 were also obtained. Surface plasmon resonance based BIA has provided invaluable kinetic information which offers insights into the mechanism of protein-DNA interactions.

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=> d his

     (FILE 'HOME' ENTERED AT 15:34:16 ON 25 OCT 2002)

     FILE 'CA' ENTERED AT 15:34:24 ON 25 OCT 2002
L1            10 S ZINC FINGER POLYPEPTIDE
L2             3 S LIBRA?(5W)ZINC(4W)FINGER(4W)(PEPTIDE OR POLYPEPTIDE OR ZIF268

=> s l1 not l2
L3            9 L1 NOT L2

=> d l3 1-9 ti au so py ab

L3   ANSWER 1 OF 9  CA  COPYRIGHT 2002 ACS
TI   Transgenic plants expressing zinc finger protein for the regulation of
     gene expression
IN   Choo, Yen; Ullman, Christopher Graeme; Chua, Nam-Hai; Sanchez, Juan Pablo
SO   U.S. Pat. Appl. Publ., 32 pp., Cont.-in-part of Appl. No. PCT/GB00/02071.
     CODEN: USXXCO
PY   2002
     2000
     2001
     2002
AB   A method is provided of regulating transcription in a plant cell from a
     DNA sequence comprising a target DNA operably linked to a coding sequence,
     which method comprises introducing an engineered zinc
     finger polypeptide in said plant cell which polypeptide
     binds to the target DNA and modulates transcription of the coding
     sequence.

L3   ANSWER 2 OF 9  CA  COPYRIGHT 2002 ACS
TI   Screening system for zinc finger polypeptides for a desired binding
     ability
IN   Choo, Yen
SO   PCT Int. Appl., 49 pp.
     CODEN: PIXXD2
PY   2000
     2001
     2002
     2002
AB   The invention relates to a method for producing a zinc finger nucleic
     acid-binding protein comprising prepg. a zinc finger protein according
     design rules, varying the protein at one or more positions, and selecting
     variants which bind to a target nucleic acid sequence by polysome display.
     The general structure of a transcription template suitable for selection
     of zinc finger polypeptides comprises a bacteriophage T7 RNA polymerase
     promoter, which drives a coding sequence encoding a zinc
     finger polypeptide. Appended to the coding sequence is
     a linker/stalling sequence region which comprises a flexible Gly/Ser
     linker, an easily translatable region, and a stalling region which is
     composed of codons rare in Escherichia coli. The polysome display method
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comprises the steps: (1) introducing a population of mRNA species into an in vitro translation system under conditions suitable for translation to form a pool of polysomes displaying nascent zinc finger polypeptides; (2) contacting the polysomes with a target nucleic acid under suitable binding conditions; (3) selecting polysomes which are specifically bound to the nucleic acid; and (4) reverse transcribing and amplifying the isolated mRNA. Often, the nucleic acid used for screening is immobilized, such as by being bound to a solid support. A further improvement to the general methods of screening nascent **zinc finger polypeptide**-displaying polysomes comprises the addnl. step of adding a preblocking agent (e.g., nonfat milk, serum albumin, tRNA, and/or gelatin) prior to or concomitant with the step of contacting the nascent peptide-displaying polysomes with an immobilized nucleic acid. The combination of a known set of rules for the design of zinc finger polypeptides, varying the protein at one or more positions, and the polysome display selection process allows the prodn. of artificial nucleic acid-binding proteins.

L3 ANSWER 3 OF 9 CA COPYRIGHT 2002 ACS
TI Imprinting of a RING zinc-finger encoding gene in the mouse chromosome region homologous to the Prader-Willi syndrome genetic region
AU Jong, Michelle T. C.; Carey, Alisoun H.; Caldwell, Kim A.; Lau, Michel H.; Handel, Mary Ann; Driscoll, Daniel J.; Stewart, Colin L.; Rinchik, Eugene M.; Nicholls, Robert D.
SO Human Molecular Genetics (1999), 8(5), 795-803
CODEN: HMGEE5; ISSN: 0964-6906
PY 1999
AB A novel locus in the human Prader-Willi syndrome (PWS) region encodes the imprinted ZNF127 and antisense ZNF127AS genes. Here, we show that the mouse ZNF127 ortholog, Zfp127, encodes a homologous putative **zinc -finger polypeptide**, with a RING (C3HC4) and three C3H zinc-finger domains that suggest function as a ribonucleoprotein. By the use of RT-PCR across an in-frame hexamer tandem repeat and RNA from a Mus musculus .times. M.spretus F1 interspecific cross, we show that Zfp127 is expressed only from the paternal allele in brain, heart and kidney. Similarly, Zfp127 is expressed in differentiated cells derived from androgenetic embryonic stem cells and normal embryos but not those from parthogenetic embryonic stem cells. We hypothesize that the gametic imprint may be set, at least in part, by the transcriptional activity of Zfp127 in pre- and post-meiotic male germ cells. Therefore, Zfp127 is a novel imprinted gene that may play a role in the imprinted phenotype of mouse models of PWS.

L3 ANSWER 4 OF 9 CA COPYRIGHT 2002 ACS
TI Interaction of the RNA binding fingers of Xenopus transcription factor IIIA with specific regions of 5 S ribosomal RNA
AU McBryant, Steven J.; Veldhoen, Nik; Gedulin, Ben; Leresche, Anne; Foster, Mark P.; Wright, Peter E.; Romaniuk, Paul J.; Gottesfeld, Joel M.
SO Journal of Molecular Biology (1995), 248(1), 44-57
CODEN: JMOBAK; ISSN: 0022-2836
PY 1995
AB Zinc fingers 4 to 7 of Xenopus transcription factor IIIA (TFIIIA) represent the minimal polypeptide necessary for high-affinity binding to 5 S rRNA. Mutations covering the entire 5 S rRNA structure were compared for their effects on the binding affinity of full-length TFIIIA and a polypeptide consisting of fingers 4 to 7 of TFIIIA (zf4-7). In addn., RNase footprinting was used to compare the binding sites of TFIIIA and zf4-7 on 5 S RNA. The consistency between the data obtained from these 2 approaches provided a clear indication that zinc fingers 4 to 7 of TFIIIA bind to a central core region on the 5 S rRNA mol. consisting of a loop B/helix II/loop A/helix V/region E. This information was used to design a truncated 75-nucleotide-long RNA mol. that retains high affinity for zf4-7. Therefore, the specific interaction of TFIIIA with 5 S rRNA can be represented by a complex formed between a four **zinc**

finger polypeptide and a truncated 5 S rRNA mol.

L3 ANSWER 5 OF 9 CA COPYRIGHT 2002 ACS
TI WT1 as a new prognostic factor and a new marker for the detection of minimal residual disease in acute leukemia
AU Inoue, Kazushi; Sugiyama, Haruo; Ogawa, Hiroyasu; Nakagawa, Masashi; Yamagami, Tamotsu; Miwa, Hiroshi; Kita, Kenkichi; Hiraoka, Akira; Masaoka, Tohru; et al.
SO Blood (1994), 84(9), 3071-9
CODEN: BLOOAW; ISSN: 0006-4971
PY 1994
AB The WT1 gene encoding a **zinc finger polypeptide** is a tumor suppressor gene that plays a key role in the carcinogenesis of Wilms' tumor. Reverse transcriptase-polymerase chain reaction (RT-PCR) was used to examine relative levels of WT1 gene expression (defined in K562 cells as 1.00) in 45 patients with acute myelogenous leukemia (AML), 22 with acute lymphocytic leukemia (ALL), 6 with acute mixed lineage leukemia (AMLL), 23 with chronic myelogenous leukemia (CML), and 24 with non-Hodgkin's lymphoma. Significant levels of WT1 gene were expressed in all leukemia patients and for CML the levels increased as the clin. phase progressed. In striking contrast with acute leukemia, the levels of WT1 gene expression for NHL were significantly lower or even undetectable. Clear correlation was obsd. between the relative levels of WT1 gene expression (<0.6 v .gtoreq.0.6) and the prognosis for acute leukemia (AML, ALL, and AMLL). Patients with less than 0.6 levels had significantly higher rates of complete remission (CR), disease-free survival, and overall survival than those with .gtoreq.0.6 levels, whereas CR could not be induced in any of the 7 patients with acute leukemia having greater than 1.0 levels of WT1 gene expression. The quantitation of the WT1 gene expression made it possible to detect minimal residual disease (MRD) in acute leukemia regardless of the presence or absence of tumor-specific DNA markers. Continuous monitoring of the WT1 mRNA was performed for 9 patients with acute leukemia. In 4 patients, MRD was detected 2 to 8 mo before clin. relapse became apparent. In 2 other patients, the WT1 mRNA gradually increased after discontinuation of chemotherapy. No MRD was detected in the remaining 3 patients with AML who received intensive induction and consolidation therapy. Simultaneous monitoring of MRD by RT-PCR using primers for specific DNA markers in 3 patients (2 AML-M3 with PML/RAR.alpha., and 1 AML-M2 with ML1/ETO) among these 9 patients detected MRD comparable with that obtained from quantitation of WT1 gene expression. In a patient with acute promyelocytic leukemia, the limits of leukemic cell detection by RT-PCR using either WT1 or promyelocytic leukemia/retinoic acid receptor-.alpha. gene primers were 10-3 to 10-4 and 10-4 for bone marrow, and 10-5 and 10-4 for peripheral blood, resp. Therefore, the authors conclude that WT1 is a new prognostic factor and a new marker for the detection of MRD in acute leukemia.

L3 ANSWER 6 OF 9 CA COPYRIGHT 2002 ACS
TI Sequence and structural requirements for high-affinity DNA binding by the WT1 gene product
AU Nakagama, Hitoshi; Heinrich, Gunther; Pelletier, Jerry; Housman, David D.
SO Molecular and Cellular Biology (1995), 15(3), 1489-98
CODEN: MCEBD4; ISSN: 0270-7306
PY 1995
AB The Wilms' tumor suppressor gene, WT1, encodes a **zinc finger polypeptide** which plays a key role regulating cell growth and differentiation in the urogenital system. Using the whole-genome PCR approach, the authors searched murine genomic DNA for high-affinity WT1 binding sites and identified a 10-bp motif 5'GCGTGGGAGT3' (which the authors term WTE). The WTE motif is similar to the consensus binding sequence 5'GCG(G/T)GGGCG3' recognized by EGR-1 and is also suggested to function as a binding site for WT1, setting up a competitive regulatory loop. To evaluate the underlying biochem. basis

for such competition, the authors compared the binding regulatory loop. To evaluate the underlying biochem. basis for such competition, the authors compared the binding affinities of WT1 and EGR1 for both sequences. WT1 shows a 20- to 30-fold-higher affinity for the WTE sequence compared with that of the EGR-1 binding motif. Mutational anal. of the WTE motif revealed a significant contribution to binding affinity by the adenine nucleotide at the eighth position (5'GCGTGGGAGT3') as well as by the 3'-most thymine (5'GCGTGGGGAGT3'), whereas mutations in either flanking nucleotides or other nucleotides in the core sequence did not significantly affect the specific binding affinity. Mutations within WT1 zinc fingers II to IV abolished the sequence-specific binding of WT1 to WTE, whereas alterations within the first WT1 zinc finger reduced the binding affinity .apprx.10-fold but did not abolish sequence recognition. The authors have thus identified a WT1 target, which, although similar in sequence to the EGR-1 motif, shows a 20- to 30-fold-higher affinity for WT1. These results suggest that physiol. action of WT1 is mediated by binding sites of significantly higher affinity than the 9-bp EGR-1 binding motif. The role of the thymine base in contributing to binding affinity is discussed in the context of recent structural anal.

L3 ANSWER 7 OF 9 CA COPYRIGHT 2002 ACS
TI Identification of the cellular protein encoded by the human Wilms' tumor (WT1) gene
AU Telerman, Adam; Dodemont, Huub; Degraef, Chantal; Galand, Paul; Bauwens, Serge; Van Oostveldt, Patrick; Amson, Robert B.
SO Oncogene (1992), 7(12), 2545-8
CODEN: ONCNES; ISSN: 0950-9232
PY 1992
AB A putative tumor-suppressor gene (wt1) located at chromosome 11p13 and involved in Wilms' tumor development has recently been identified as a **zinc finger polypeptide**-encoding gene. The purpose of this study was to characterize the protein encoded by the human wt1 gene. The region spanning the entire zinc finger domain was amplified by polymerase chain reaction (PCR) and subcloned in the pATH 3 expression vector. Polyclonal antibodies against the fused TrpE-WT protein were raised. These antibodies immunopptd. a 49- to 51-kDa protein from hematopoietic tumor cells labeled in vivo with [35S]methionine. Subcellular fractionation and immunohistochem. followed by confocal microscopy indicated that the Wilms' tumor gene product (WT1) is mainly localized within the nucleus.

L3 ANSWER 8 OF 9 CA COPYRIGHT 2002 ACS
TI Isolation, characterization, and expression of the murine Wilms' tumor gene (WT1) during kidney development
AU Buckler, Alan J.; Pelletier, Jerry; Haber, Daniel A.; Glaser, Tom; Housman, David E.
SO Molecular and Cellular Biology (1991), 11(3), 1707-12
CODEN: MCEBD4; ISSN: 0270-7306
PY 1991
AB The human Wilms' tumor predisposition gene, WT1, is a Cys-His **zinc finger polypeptide** which appears to be a transcription factor controlling gene expression during embryonic kidney development. To analyze the role of the WT1 gene in nephroblast differentiation, the murine homolog of human WT1 was isolated. An extremely high level of amino acid sequence conservation (>95%) extends throughout all regions of the predicted mouse and human WT1 polypeptides. Two alternative splices within the WT1 transcript have been conserved between mice and humans suggesting that these have functional significance. Expression of the mouse WT1 mRNA in fetal kidney increases during late gestation, peaks just prior to or shortly after birth, and declines dramatically by 15 days postpartum. Developmental regulation of WT1 expression appears to be selective for the kidney. The restriction of WT1 expression to a limited no. of tissues is in contrast to previously described tumor suppressor genes. In addn., the narrow window of time during which WT1 is expressed

at high levels in the kidney is consistent with the origin of Wilms' tumor from primitive nephroblasts and the postulated role of this gene as a neg. regulator of growth.

L3 ANSWER 9 OF 9 CA COPYRIGHT 2002 ACS
TI Isolation and characterization of a **zinc finger polypeptide** gene at the human chromosome 11 Wilms' tumor locus
AU Call, Katherine M.; Glaser, Tom; Ito, Caryn Y.; Buckler, Alan J.; Pelletier, Jerry; Haber, Daniel A.; Rose, Elise A.; Kral, Astrid; Yeger, Herman; et al.
SO Cell (Cambridge, MA, United States) (1990), 60(3), 509-20
CODEN: CELLB5; ISSN: 0092-8674
PY 1990
AB The authors isolated a series of genomic and cDNA clones mapping within the boundaries of constitutional and tumor deletions that define the Wilms' tumor locus on human chromosome 11 (band p13). The transcription unit corresponding to these clones spans approx. 50 kb and encodes an mRNA approx. 3 kb long. This mRNA is expressed in a limited range of cell types, predominantly in the kidney and a subset of hematopoietic cells. The polypeptide encoded by this locus has a no. of features suggesting a potential role in transcriptional regulation. These include the presence of four zinc finger domains and a region rich in proline and glutamine. The amino acid sequence of the predicted polypeptide shows significant homol. to two growth regulated mammalian polypeptides, EGR1 and EGR2. The genetic localization of this gene, its tissue-specific expression, and the function predicted from its sequence suggest that it represents the 11p13 Wilms' tumor gene.

```
=> s overlap?(5w)random(5w)(peptide or polypeptide)
         80154 OVERLAP?
        108050 RANDOM
        273453 PEPTIDE
         86733 POLYPEPTIDE
L4           0 OVERLAP?(5W)RANDOM(5W)(PEPTIDE OR POLYPEPTIDE)

=> s overlap(5w)random(4w)peptide
         36860 OVERLAP
        108050 RANDOM
        273453 PEPTIDE
L5           0 OVERLAP(5W)RANDOM(4W)PEPTIDE

=> s tandem
L6       31651 TANDEM

=> s l6 and overlap
         36860 OVERLAP
L7         131 L6 AND OVERLAP

=> s l7 and random
        108050 RANDOM
L8           2 L7 AND RANDOM

=> d l8 1-2 ti au so py ab

L8 ANSWER 1 OF 2 CA COPYRIGHT 2002 ACS
TI Characteristic enrichment of DNA repeats in different genomes
AU Cox, Randal; Mirkin, Sergei M.
SO Proceedings of the National Academy of Sciences of the United States of America (1997), 94(10), h5237-5242
CODEN: PNASA6; ISSN: 0027-8424
PY 1997
AB Using computer programs developed for this purpose, we searched for various repeated sequences including inverted, direct tandem,
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